AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

LISTING OF CLAIMS:

1. (Currently Amended) An isolated nucleic acid sequence of SEQ ID NO: ~~2~~ 1.

2. (Original) The isolated nucleic acid sequence of claim 1, wherein the nucleic acid sequence is DNA.

3. (Canceled)

4. (Currently Amended) [[A]] An isolated nucleic acid sequence encoding the amino acid sequence of SEQ ID NO: [[4]] 3.

5. (Currently Amended) A replicative cloning vector comprising the nucleic acid sequence of claim [[1]] 4 and a replicon operative in an isolated host cell.

6. (Original) An isolated host cell transformed with the replicative cloning vector of claim 5.

7. (Currently Amended) An expression vector comprising the nucleic acid sequence of claim [[1]] 4 operably linked to a transcription regulatory region.

8. (Original) An isolated host cell transformed with the expression vector of claim 7.

9-13 (Canceled)

14. (Original) A method for identifying a protein involved in bone modulation comprising identifying a protein that has an expression level that is different in a first host comprising the Zmax1 gene when compared to a second host comprising the HBM gene.

15. (Original) The method of claim 14, wherein the host is a cell or an animal.

16-21. (Canceled)

22. (Currently Amended) A method for identification of a candidate molecule involved in bone modulation comprising

identifying a first molecule that binds to, or that inhibits binding of a second molecule to, the nucleic acid sequence of SEQ ID NO: 1;

identifying ~~[[a]]~~ whether the first molecule ~~[[that]]~~ binds to, or ~~[[that]]~~ inhibits binding of ~~[[a]]~~ the second molecule to, the nucleic acid sequence of SEQ ID NO: 2; and

comparing the extent of binding, or the extent of inhibition of binding, of the first molecule to each nucleic acid sequence, wherein the molecule that binds, or inhibits binding, more or less to the nucleic acid sequence of SEQ ID NO: 2 or the nucleic acid sequence of SEQ ID NO: 1 is the candidate molecule.

23. (Original) The method of claim 22, wherein the candidate molecule is a protein or an mRNA.

24. (Original) A method of pharmaceutical development for treatment of bone development disorders comprising identifying a molecule that binds to the amino acid sequence of SEQ ID NO: [[4]] 2.

25. (Original) The method of claim 24, wherein the molecule inhibits or enhances the function of the amino acid.

26. (Original) A method of pharmaceutical development for treatment of bone development disorders comprising

constructing a first host that contains the Zmax1 gene or protein;

constructing a second host that contains the HBM gene or protein;

analyzing a difference between the first host and the second host;

identifying a molecule that, when added to the first host, causes the first host to exhibit a characteristic feature of the second host.

27. (Original) The method of claim 26, wherein the host is a cell-free extract, a cell or an animal.

28-42 (Canceled)

43. (Original) A method for treating bone development disorders comprising administering a molecule that binds to the nucleic acid sequence of claim 1 to a patient in need thereof.

44. (Original) The method of claim 43, wherein the patient is a human or a bird.

45-74. (Canceled)

75. (New) An isolated nucleic acid of at least 15 contiguous nucleotides capable of hybridizing under stringent conditions to a target sequence comprising the reverse complement of SEQ ID NO: 8 and SEQ ID NO: 9, or the complement of said target sequence, wherein the nucleic acid includes a polymorphic site selected from the group consisting of:

wherein nucleotide 69169 of SEQ ID NO: 9 is replaced by A,

wherein nucleotide 27402 of SEQ ID NO: 9 is replaced by G,

wherein nucleotide 27841 of SEQ ID NO: 9 is replaced by C,

wherein nucleotide 35600 of SEQ ID NO: 9 is replaced by G,

wherein nucleotide 45619 of SEQ ID NO: 9 is replaced by A,

wherein nucleotide 46018 of SEQ ID NO: 9 is replaced by G,

wherein nucleotide 46093 of SEQ ID NO: 9 is replaced by G,

wherein nucleotide 46190 of SEQ ID NO: 9 is replaced by G,

wherein nucleotide 50993 of SEQ ID NO: 9 is replaced by C,

wherein nucleotide 51124 of SEQ ID NO: 9 is replaced by T,

wherein nucleotide 55461 of SEQ ID NO: 9 is replaced by T,

wherein nucleotide 63645 of SEQ ID NO: 9 is replaced by A,

wherein nucleotide 63646 of SEQ ID NO: 9 is replaced by C,

wherein nucleotide 24809 of SEQ ID NO: 9 is replaced by G,

wherein nucleotide 27837 of SEQ ID NO: 9 is replaced by C,

wherein nucleotide 31485 of SEQ ID NO: 9 is replaced by T,

wherein nucleotide 31683 of SEQ ID NO: 9 is replaced by G,

wherein nucleotide 24808 of SEQ ID NO: 9 is replaced by G,

wherein nucleotide 31340 of SEQ ID NO: 8 is replaced by C,

wherein nucleotide 32538 of SEQ ID NO: 8 is replaced by G,

wherein nucleotide 13224 of SEQ ID NO: 8 is replaced by G,

wherein nucleotide 21119 of SEQ ID NO: 8 is replaced by A,

wherein nucleotide 30497 of SEQ ID NO: 8 is replaced by A,

wherein nucleotide 24811 of SEQ ID NO: 9 is replaced by C, and

wherein nucleotide 68280 of SEQ ID NO: 9 is replaced by A.

76. (New) The isolated nucleic acid segment of claim 75, wherein nucleotide 21119 of SEQ ID NO: 8 is replaced by A.

77. (New) The isolated nucleic acid of claim 75 that is DNA.

78. (New) The isolated nucleic acid of claim 75 that is RNA.

79. (New) A probe comprising the isolated nucleic acid of claim 75.

80. (New) A method for identification of a candidate molecule involved in bone modulation comprising

identifying a first molecule that binds to, or that inhibits binding of a second molecule to, the nucleic acid sequence of SEQ ID NO: 1.